

PCT09

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/889,592

DATE: 12/19/2001
 TIME: 15.56.34

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7 <110> APPLICANT: Ingvar M. Ferby et al.
 13 <120> TITLE OF INVENTION: PROTEIN WITH CELL PROLIFERATION AND CELL DIVISION
 14 MODULATING ACTIVITY AND DNA ENCODING SUCH PROTEIN
 20 <130> FILE REFERENCE: 100561-00064
 26 <140> CURRENT APPLICATION NUMBER: 09/889,592
 C--> 29 <141> CURRENT FILING DATE: 2001-10-31
 35 <150> PRIOR APPLICATION NUMBER: PCT/EP00/00877
 38 <151> PRIOR FILING DATE: 2000-02-03
 44 <150> PRIOR APPLICATION NUMBER: EP 99102172.6
 47 <151> PRIOR FILING DATE: 1999-02-03
 53 <160> NUMBER OF SEQ ID NOS: 4
 59 <170> SOFTWARE: Patent-In version 3.1
 65 <210> SEQ ID NO: 1
 68 <211> LENGTH: 1575
 71 <212> TYPE: DNA
 74 <213> ORGANISM: Xenopus sp.
 80 <220> FEATURE:
 83 <221> NAME/KEY: CDS
 86 <222> LOCATION: (211)..(211..3)
 89 <223> OTHER INFORMATION:
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 102 ttttttatta ttccaggagg ctataaagag agcagacaaa ggaagtaggc ggagttcctg 120
 106 ttatcgcca tttggccagt ggtggctaag cgcctgaagg tggctgcttc ctttgctcag 180
 110 atcaaccctc gggccggtgt cccctttct aca atg agg cac atg cag agt gta 234
 112 Met Arg His Met Gln Ser Val
 114 1 5
 118 acc cgg gcc age tcc att tgt ggc agc ggg gtg aag cag gtc att ggc 282
 120 Thr Arg Ala Ser Ser Ile Cys Gly Ser Gly Val Lys Gln Val Ile Gly
 122 10 15 20
 126 aag ggg cat ccg cac gcc cgg gtt gtt gga gcg cgc aag gcg caa atc 330
 128 Lys Gly His Pro His Ala Arg Val Val Gly Ala Arg Lys Ala Gln Ile
 130 25 30 35
 134 cct gag aqa gag gag ttg tca qtc aaa ccc aaa atg qtq cqa aat acc 378
 136 Pro Glu Arg Glu Glu Leu Ser Val Lys Pro Lys Met Val Arg Asn Thr
 138 40 45 50 55
 142 cat ctc aat cta cag ccc cag gag cgc cag gcc ttc tac agy ctc cta 426
 144 His Leu Asn Leu Gln Pro Gln Glu Arg Gln Ala Phe Tyr Arg Leu Leu
 146 60 65 70
 150 gaa aat gag cag att cag gaa ttc ctt tct atg gac tcc tgt cta aag 474
 152 Glu Asn Glu Gln Ile Gln Glu Phe Leu Ser Met Asp Ser Cys Leu Arg
 154 75 80 85
 158 att tcc gac aag tat ctc ata gca atg gtt cta gca tat ttt aag cgg 522
 160 Ile Ser Asp Lys Tyr Leu Ile Ala Met Val Leu Ala Tyr Phe Lys Arg
 162 90 95 100
 166 gca gcg ggc ctc tac acc agc gag tac aca acc atg aat ttc ttt gtt 570
 168 Ala Ala Gly Leu Tyr Thr Ser Glu Tyr Thr Thr Met Asn Phe Phe Val

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170      105      110      115
174 gcc ctg tat ctg gct aat gac atg gag gaa gat qaa gaa gac tat aaa      618
176 Ala Leu Tyr Leu Ala Asn Asp Met Glu Glu Asp Glu Glu Asp Tyr Lys
178 120      125      130      135
182 tat gaa atc ttc ccc tgg gca cta gga gac tgg tgg cgt gag ctt ttc      666
184 Tyr Glu Ile Phe Pro Trp Ala Leu Gly Asp Ser Trp Arg Glu Leu Phe
186      140      145      150
190 cca caa ttt ttg cgt ctc cgg gac gac ttc tgg gct aaa atg aac tac      714
192 Pro Gln Phe Leu Arg Leu Arg Asp Asp Phe Trp Ala Lys Met Asn Tyr
194      155      160      165
198 cga gca gtt gtt agt cga aag tgc tgt gat gag gta atg tcc aaa gat      762
200 Arg Ala Val Val Ser Arg Arg Cys Lys Asp Glu Val Met Ser Lys Asp
202      170      175      180
206 ccc act cat tgg gcc tgg ctg aga tat cgc ccc atg cat cac agc ggg      810
208 Pro Thr His Trp Ala Trp Leu Arg Asp Arg Pro Met His His Ser Gly
210      185      190      195
214 gcc atg cgt ggt tac ctt aga aac gag gac gac ttt ttc ccc cgg ggt      858
216 Ala Met Arg Gly Tyr Leu Arg Asn Glu Asp Asp Phe Phe Pro Arg Gly
218 200      205      210      215
222 cca ggc ctt aca cca gcc agc tgt aca ctt tac cat aaa gca ggt gtc      906
224 Pro Gly Leu Thr Pro Ala Ser Lys Thr Leu Lys His Lys Ala Gly Val
226      220      225      230
230 tat gat tat gat tgg gtc tcc tac tcc tcc tat tcc tat cca gaa caa      954
232 Cys Asp Ser Gly Gly Val Ser His Asn Asn Ser Ser Ser Pro Glu Gln
234      235      240      245
238 gag att ttt cac tac acc aat agg gag tgg tcc cag gag ctt ctc atg      1002
240 Glu Ile Phe His Tyr Thr Asn Arg Glu Trp Ser Gln Glu Leu Leu Met
242      250      255      260
246 ttg ccc cct gag ctg ttg ctg gat ccc gag tgt act cat gac tta cac      1050
248 Leu Pro Pro Glu Leu Leu Leu Asp Pro Glu Cys Thr His Asp Leu His
250      265      270      275
254 att ctc cag gag cca ttg gtt gga tta gag cca gat ggg acg gcg ctg      1098
256 Ile Leu Gln Glu Pro Leu Val Gly Leu Glu Pro Asp Gly Thr Ala Leu
258 280      285      290      295
262 gaa tgg cac cac ctt tagtagccga ttgtctctctc cgagcttitta ttctctctc      1153
264 Glu Trp His His Leu
266      300
270 cccacaagct cagcaattat tctctctctcc taaggacttg tcaatgttca gacttaattc      1113
272 aaatgggaga agtgaatatt ccgacgggatg tagagcggga atatgtgccc agagaaagtg      1173
274 ttttqagtct gtataaacgg ttgcttttga aataaatata taaatgttct ctgtgctggt      1333
276 cacttaataa gatcagataa aatcaatttc aagtataatt taatagtatg tatgtagaat      1393
278 cttaattca gctctccacc aaatagtaac ttgtcatcac tgaacctttg cttaactaca      1453
280 cttaattat ttgcaacaca aatattctga aatcagacc attctatttt cagatgaatt      1513
282 gaaaatatta aactcaacag aattctgtg gtgtaattga aatgcaaaga tcgattagac      1573
284 ta
304 <210> SEQ ID NO: 2
307 <211> LENGTH: 300
310 <212> TYPE: PRT
313 <213> ORGANISM: Xenopus sp

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319 <400> SEQUENCE: 2

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323 Met Arg His Met Gln Ser Val Thr Arg Ala Ser Ser Ile Cys Gly Ser
325 1 5 10 15
331 Gly Val Lys Gln Val Ile Gly Lys Gly His Pro His Ala Arg Val Val
333 20 25 30
339 Gly Ala Arg Lys Ala Gln Ile Pro Glu Arg Glu Glu Leu Ser Val Lys
341 35 40 45
347 Pro Lys Met Val Arg Asn Thr His Leu Asn Leu Gln Pro Gln Glu Arg
349 50 55 60
355 Gln Ala Phe Tyr Arg Leu Leu Glu Asn Glu Gln Ile Gln Glu Phe Leu
357 65 70 75 80
363 Ser Met Asp Ser Cys Leu Arg Ile Ser Asp Lys Tyr Leu Ile Ala Met
365 85 90 95
371 Val Leu Ala Tyr Phe Lys Arg Ala Ala Gly Leu Tyr Thr Ser Glu Tyr
373 100 105 110
379 Thr Thr Met Asn Phe Phe Val Ala Leu Tyr Leu Ala Asn Asp Met Glu
381 115 120 125
387 Glu Asp Glu Glu Asp Tyr Lys Tyr Glu Ile Phe Pro Trp Ala Leu Gly
389 130 135 140
395 Asp Ser Trp Arg Glu Leu Phe Pro Gln Phe Leu Arg Leu Arg Asp Asp
397 145 150 155 160
403 Phe Trp Ala Lys Met Asn Tyr Arg Ala Val Val Ser Arg Arg Cys Cys
405 165 170 175
411 Asp Glu Val Met Ser Lys Asp Pro Thr His Trp Ala Trp Leu Arg Asp
413 180 185 190
419 Arg Pro Met His His Ser Gly Ala Met Arg Gly Tyr Leu Arg Asn Glu
421 195 200 205
427 Asp Asp Phe Phe Pro Arg Gly Pro Gly Leu Thr Pro Ala Ser Cys Thr
429 210 215 220
435 Leu Cys His Lys Ala Gly Val Cys Asp Ser Gly Gly Val Ser His Asn
437 225 230 235 240
443 Asn Ser Ser Ser Pro Glu Gln Glu Ile Phe His Tyr Thr Asn Arg Glu
445 245 250 255
451 Trp Ser Gln Glu Leu Leu Met Leu Pro Pro Glu Leu Leu Leu Asp Pro
453 260 265 270
459 Glu Cys Thr His Asp Leu His Ile Leu Gln Glu Pro Leu Val Gly Leu
461 275 280 285
467 Glu Pro Asp Gly Thr Ala Leu Glu Trp His His Leu
469 290 295 300

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477 <210> SEQ ID NO: 3

480 <211> LENGTH: 1357

483 <212> TYPE: DNA

486 <213> ORGANISM: Xenopus sp.

492 <220> FEATURE:

495 <221> NAME/KEY: CDS

498 <222> LOCATION: (163)..(1056)

501 <223> OTHER INFORMATION:

508 <400> SEQUENCE: 3

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510 gctgtatttt actttctttt aggaaggetat aaagacaaca gacaggggag gtaggcagag 60

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514 ttctctgttca tcaacattct ttggccgttg gtgqctaggg qoctqaaqgt qoctqctacc 120
518 ttgctcaga tcaacccctcg gttcgttgic cccctttcta ca atg agg cat atg 174
520 Met Arg His Met
522 1
526 caq agt gca acc cgg gcc acc tta gtt tgt ggc agc ggg gta aag cag 222
528 Gln Ser Ala Thr Arg Ala Thr Leu Val Cys Gly Ser Gly Val Lys Gln
530 5 10 15 20
534 atc att gcc aag gga cat ccg aat acc cgg gtt ttt gga gcg cgc aag 270
536 Ile Ile Ala Lys Gly His Pro Asn Thr Arg Val Phe Gly Ala Arg Lys
538 25 30 35
542 gcg aaa atc cct gag aga gag gtg cta gca gcc aaa ccc aag atc acg 318
544 Ala Lys Ile Pro Glu Arg Glu Val Leu Ala Ala Lys Pro Lys Ile Thr
546 40 45 50
550 cgc att aca cat ctc aat cta caa ccc cag gag cgc cag gcc ttt tac 366
552 Arg Ile Thr His Leu Asn Leu Gln Pro Gln Glu Arg Gln Ala Phe Tyr
554 55 60 65
558 agg ctc cta gaa aat gag ctg att cag gaa ttt ctt tct atg gac tcc 414
560 Arg Leu Leu Glu Asn Glu Leu Ile Gln Glu Phe Leu Ser Met Asp Ser
562 70 75 80
566 tgt cta aag att tca gac aag tat ctc ata gca atg gtt cta gca tat 462
568 Cys Leu Lys Ile Ser Asp Lys Tyr Leu Ile Ala Met Val Leu Ala Tyr
570 85 90 95 100
574 ttt aag cag gcc gcc ctc tac acc gcc ggg ttc acc acc atg aat ttc 510
576 Phe Lys Arg Ala Gly Leu Tyr Thr Ser Glu Tyr Thr Thr Met Asn Phe
578 105 110 115
582 ttt gtt gct ctg tat ctg gct aat gac atg gag gaa gat gaa gaa gac 558
584 Phe Val Ala Leu Tyr Leu Ala Asn Asp Met Glu Glu Asp Glu Glu Asp
586 120 125 130
590 tat aaa tat gaa atc ttc ccc tgg gca cta gga gat tca tgg cgt gag 606
592 Tyr Lys Tyr Glu Ile Phe Pro Trp Ala Leu Gly Asp Ser Trp Arg Glu
594 135 140 145
598 ttt ttc cca caa ttt tta cgt ctc cgg gac gac ttc tgg gct aaa atg 654
600 Phe Phe Pro Gln Phe Leu Arg Leu Arg Asp Asp Phe Trp Ala Lys Met
602 150 155 160
606 aac tac cga gca gtt gtt agc cga aga tgt tgt gat gag gta atg gcg 702
608 Asn Tyr Arg Ala Val Val Ser Arg Arg Cys Cys Asp Glu Val Met Ala
610 165 170 175 180
614 aaa gat ccc act cat tgg gcc tgg ctc aga gat cgt cct att cat cat 750
616 Lys Asp Pro Thr His Trp Ala Trp Leu Arg Asp Arg Pro Ile His His
618 185 190 195
622 agt ggg gcc ctg cgt ggt tac ctc aga aat gaa gat gac ttt ttc cct 798
624 Ser Gly Ala Leu Arg Gly Tyr Leu Arg Asn Glu Asp Asp Phe Phe Pro
626 200 205 210
630 cgg ggt cca ggc ctt aca cca gcc agc tgt gca ctt tgc cat aaa gca 846
632 Arg Gly Pro Gly Leu Thr Pro Ala Ser Cys Ala Leu Cys His Lys Ala
634 215 220 225
638 agt gtc tgt gac tct ggt ggg gtg tcc cat gac aac tct tct cca gaa 894
640 Ser Val Cys Asp Ser Gly Gly Val Ser His Asp Asn Ser Ser Pro Glu
642 230 235 240

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646 caa gag att ttt cac tac acc aat agg gag tgg tcc cag gaa ctt ctc      942
648 Gln Glu Ile Phe His Tyr Thr Asn Arg Gln Trp Ser Gln Glu Leu Leu
650 245                250                255                260
654 atc ttg cca cct gaa ctg tta ttg gat cgg gag tct act tat gac atc      990
656 Ile Leu Pro Pro Glu Leu Leu Leu Asp Pro Glu Ser Thr Tyr Asp Ile
658                265                270                275
662 cac att ttc cag gaa cgg ttg gtt gga tta gag cca gat gag gca gcc      1038
664 His Ile Phe Gln Glu Pro Leu Val Gly Leu Glu Pro Asp Gly Ala Ala
666                280                285                290
670 ttg gaa tgg cac cac ctt tagcaccatg tcatctctgt gctttcattc      1086
672 Leu Glu Trp His His Leu
674                295
678 ttctctaatc caccagctca agaagcaatt aacctctctt aaqcaattgc ccatgtccct      1146
682 attcagacta atgaattaaa tgggagaggt gactattg c ataaagggaa ggatgccact      1206
686 taqagtggag aataatactt gccaaaaatg atgtttgggt ctgttttaaa tgttgctatt      1266
690 acagttgcct tgtaaataaa taagtataaa atgtatgct ctgtgcgggt tgctaataaa      1326
694 aaaaaaatct ggtatcaaaa aaaaaaaaaa a
696                1357
700 <210> SEQ ID NO: 4
702 <211> LENGTH: 298
704 <212> TYPE: PRT
706 <213> ORGANISM: Xenopus sp.
708 <400> SEQUENCE: 4
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726                20                25                30
732 Gly Ala Arg Lys Ala Lys Ile Pro Glu Arg Glu Val Leu Ala Ala Lys
734                35                40                45
740 Pro Lys Ile Thr Arg Ile Thr His Leu Asn Leu Gln Pro Gln Glu Arg
742                50                55                60
748 Gln Ala Phe Tyr Arg Leu Leu Glu Asn Glu Leu Ile Gln Glu Phe Leu
750 65                70                75                80
756 Ser Met Asp Ser Cys Leu Lys Ile Ser Asp Lys Tyr Leu Ile Ala Met
758                85                90                95
764 Val Leu Ala Tyr Phe Lys Arg Ala Gly Leu Tyr Thr Ser Glu Tyr Thr
766                100               105               110
772 Thr Met Asn Phe Phe Val Ala Leu Tyr Leu Ala Asn Asp Met Glu Glu
774                115               120               125
780 Asp Glu Glu Asp Tyr Lys Tyr Glu Ile Phe Pro Trp Ala Leu Gly Asp
782                130               135               140
788 Ser Trp Arg Glu Phe Phe Pro Gln Phe Leu Arg Leu Arg Asp Asp Phe
790 145               150               155               160
796 Trp Ala Lys Met Asn Tyr Arg Ala Val Val Ser Arg Arg Cys Cys Asp
798                165               170               175
804 Glu Val Met Ala Lys Asp Pro Thr His Trp Ala Trp Leu Arg Asp Arg
806                180               185               190
812 Pro Ile His His Ser Gly Ala Leu Arg Gly Tyr Leu Arg Asn Glu Asp
814                195               200               205
820 Asp Phe Phe Pro Arg Gly Pro Gly Leu Thr Pro Ala Ser Cys Ala Leu

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VERIFICATION SUMMARY

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L:29 M:271 C: Current Filing Date differs. Replaced Current Filing Date